

SEQUENCE LISTING

<110> Emtage, Peter C.R.

<120> METHODS OF IMMUNOTHERAPY AND DIAGNOSIS USING TARGETING OF CELLS THAT EXPRESS LAX

<130> HYS-67/PCT

<140> 2003-11-25

<141> NOT YET ASSIGNED

<150> 10/304,234

<151> 2002-11-26

<150> 10/128,558

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<150> 60/339,453

<151> 2001-12-11

<160> 8

<170> PatentIn version 3.1

<210> 1

<211> 2071

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (440)..(1636)

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gtttccccct ctgtgcccct cacgtttcca ccagaaacgt gaaggcagag gccacagatt 180
ctccctgagc cacctcaatt ggaagcacca tgtccggatg agatcgcact tcctgcagtg 240
ggcattagcc acgtccaggt agaaccaaac ctgttgcttt tgtatgttgg gtcaacttgg 300
cctgacgttt cagaggtaga cacgagatag ggagttggaa gcaggatgtc cggatgagat 360
cgcaattcct gcagagggca ttatcgccg agaaacttag aagctgaagc cagagagcat 420
ctcaaagggtt cctgataca atg gat ggt gtc act cca acc ctt tcg aca atc 472
Met Asp Gly Val Thr Pro Thr Leu Ser Thr Ile
1 5 10
aga ggg agg acc ttg gag tcc agc act ctg cat gtg act ccc cgc agc 520
Arg Gly Arg Thr Leu Glu Ser Ser Thr Leu His Val Thr Pro Arg Ser

| | |
|---|------|
| ctg gac aga aat aaa gac cag atc acc aac atc ttt tcc ggg ttt gcg Leu Asp Arg Asn Lys Asp Gln Ile Thr Asn Ile Phe Ser Gly Phe Ala 30 35 40 | 568 |
| gga ctc ctc gcc atc ctc ctg gtc gtt gcg gtt ttc tgc atc ttg tgg Gly Leu Leu Ala Ile Leu Leu Val Val Ala Val Phe Cys Ile Leu Trp 45 50 55 | 616 |
| aat tgg aat aaa cgg aag aag cga caa gtt cct tac ctc cga gtt acc Asn Trp Asn Lys Arg Lys Arg Gln Val Pro Tyr Leu Arg Val Thr 60 65 70 75 | 664 |
| gtc atg ccc ttg ctg act ttg cca caa acc aga caa aga gcc aaa aat Val Met Pro Leu Leu Thr Leu Pro Gln Thr Arg Gln Arg Ala Lys Asn 80 85 90 | 712 |
| att tat gac atc ttg cct tgg cga cag gaa gac ctg ggg aga cat gag Ile Tyr Asp Ile Leu Pro Trp Arg Gln Glu Asp Leu Gly Arg His Glu 95 100 105 | 760 |
| tcg agg agt atg cgc att ttc agt act gag agc ctc ctc tcc aga aat Ser Arg Ser Met Arg Ile Phe Ser Thr Glu Ser Leu Leu Ser Arg Asn 110 115 120 | 808 |
| tct gag agc ccg gag cat gtg ccc tcc caa gca ggc aat gcc ttc cag Ser Glu Ser Pro Glu His Val Pro Ser Gln Ala Gly Asn Ala Phe Gln 125 130 135 | 856 |
| gag cat aca gcc cac atc cat gcc aca gag tac gcg gtg ggt atc tat Glu His Thr Ala His Ile Ala Thr Glu Tyr Ala Val Gly Ile Tyr 140 145 150 155 | 904 |
| gac aac gcc atg gtc ccc cag atg tgt ggg aac ctc act ccc tcg gca Asp Asn Ala Met Val Pro Gln Met Cys Gly Asn Leu Thr Pro Ser Ala 160 165 170 | 952 |
| cac tgc atc aat gtc aga gct tcc aga gac tgc gca agc att tct tca His Cys Ile Asn Val Arg Ala Ser Arg Asp Cys Ala Ser Ile Ser Ser 175 180 185 | 1000 |
| gag gat tcg cat gat tat gtc aat gtc ccc aca gca gaa gag att gct Glu Asp Ser His Asp Tyr Val Asn Val Pro Thr Ala Glu Glu Ile Ala 190 195 200 | 1048 |
| gag act cta gct tct acc aaa agc cct tcc aga aat ctc ttt gtt ctt Glu Thr Leu Ala Ser Thr Lys Ser Pro Ser Arg Asn Leu Phe Val Leu 205 210 215 | 1096 |
| ccc agt acc cag aag ctg gag ttt act gag gaa aga gat gag ggc tgt Pro Ser Thr Gln Lys Leu Glu Phe Thr Glu Glu Arg Asp Glu Gly Cys 220 225 230 235 | 1144 |
| gga gat gct ggt gac tgc acc agt ttg tat tct cca gga gct gag gac Gly Asp Ala Gly Asp Cys Thr Ser Leu Tyr Ser Pro Gly Ala Glu Asp 240 245 250 | 1192 |
| agt gat tca ctc agc aat gga gaa ggt tct tct cag atc tca aat gac | 1240 |

| | | |
|--|-----|------|
| Ser Asp Ser Leu Ser Asn Gly Glu Gly Ser Ser Gln Ile Ser Asn Asp | | |
| 255 | 260 | 265 |
| | | |
| tat gtc aac atg aca ggg ttg gat ctc agt gcc atc cag gaa agg cag | | 1288 |
| Tyr Val Asn Met Thr Gly Leu Asp Leu Ser Ala Ile Gln Glu Arg Gln | | |
| 270 | 275 | 280 |
| | | |
| ctc tgg gtg gct ttt cag tgc tgc aga gac tat gaa aat gtt cca gca | | 1336 |
| Leu Trp Val Ala Phe Gln Cys Cys Arg Asp Tyr Glu Asn Val Pro Ala | | |
| 285 | 290 | 295 |
| | | |
| gca gat ccc agt gga agc cag cag gct gag aaa gat gtg cca tcc | | 1384 |
| Ala Asp Pro Ser Gly Ser Gln Gln Ala Glu Lys Asp Val Pro Ser | | |
| 300 | 305 | 310 |
| | | |
| tca aac ata ggt cat gtc gag gac aag aca gat gat ccc ggg acc cat | | 1432 |
| Ser Asn Ile Gly His Val Glu Asp Lys Thr Asp Asp Pro Gly Thr His | | |
| 320 | 325 | 330 |
| | | |
| gtc caa tgt gtc aaa agg aca ttc ctt gct tca ggg gat tat gca gac | | 1480 |
| Val Gln Cys Val Lys Arg Thr Phe Leu Ala Ser Gly Asp Tyr Ala Asp | | |
| 335 | 340 | 345 |
| | | |
| ttt cag cca ttc aca cag agt gag gac agt cag atg aaa cat aga gaa | | 1528 |
| Phe Gln Pro Phe Thr Gln Ser Glu Asp Ser Gln Met Lys His Arg Glu | | |
| 350 | 355 | 360 |
| | | |
| gag atg tca aat gag gac tcc agt gac tat gaa aat gtg cta act gcc | | 1576 |
| Glu Met Ser Asn Glu Asp Ser Ser Asp Tyr Glu Asn Val Leu Thr Ala | | |
| 365 | 370 | 375 |
| | | |
| aag tta gga ggc agg gac tct gag cag ggg cct ggc act cag ctc ctt | | 1624 |
| Lys Leu Gly Gly Arg Asp Ser Glu Gln Gly Pro Gly Thr Gln Leu Leu | | |
| 380 | 385 | 390 |
| | | |
| cct gat gaa tga agacccaggt acccagccat aaagccacat tgagtagtct | | 1676 |
| Pro Asp Glu | | |
| | | |
| atcccatagg attgactact gcagagtcta gtgcagaccc gtgatcacct tagtgcttca | | 1736 |
| gtggattcac tggtagatt aaaaagaggc tgagatgagc agtgaactaa gaggccacac | | 1796 |
| aaaagcagag gtttggaaat tccagaaggg aattcttctc aagcagagtg tggtatctc | | 1856 |
| ctgtaccagc ctaagaatgt ttgctgaaac tgcttcttag aactgtgaag aaagcagggaa | | 1916 |
| agtagtgcac agtagtctaa gattattacc ttcattaata ccaacaggct gcaaagcaag | | 1976 |
| agtagatatttattgtataat ccagtcagag gtcaaaagga aggaagaagt tggagtggag | | 2036 |
| tgggggtgggc aatttccatt taaaagagtg taggc | | 2071 |

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Glu Ser Ser Thr Leu His Val Thr Pro Arg Ser Leu Asp Arg Asn Lys
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Asp Gln Ile Thr Asn Ile Phe Ser Gly Phe Ala Gly Leu Leu Ala Ile
35 40 45

Leu Leu Val Val Ala Val Phe Cys Ile Leu Trp Asn Trp Asn Lys Arg
50 55 60

Lys Lys Arg Gln Val Pro Tyr Leu Arg Val Thr Val Met Pro Leu Leu
65 70 75 80

Thr Leu Pro Gln Thr Arg Gln Arg Ala Lys Asn Ile Tyr Asp Ile Leu
85 90 95

Pro Trp Arg Gln Glu Asp Leu Gly Arg His Glu Ser Arg Ser Met Arg
100 105 110

Ile Phe Ser Thr Glu Ser Leu Leu Ser Arg Asn Ser Glu Ser Pro Glu
115 120 125

His Val Pro Ser Gln Ala Gly Asn Ala Phe Gln Glu His Thr Ala His
130 135 140

Ile His Ala Thr Glu Tyr Ala Val Gly Ile Tyr Asp Asn Ala Met Val
145 150 155 160

Pro Gln Met Cys Gly Asn Leu Thr Pro Ser Ala His Cys Ile Asn Val
165 170 175

Arg Ala Ser Arg Asp Cys Ala Ser Ile Ser Ser Glu Asp Ser His Asp
180 185 190

Tyr Val Asn Val Pro Thr Ala Glu Glu Ile Ala Glu Thr Leu Ala Ser
195 200 205

Thr Lys Ser Pro Ser Arg Asn Leu Phe Val Leu Pro Ser Thr Gln Lys
210 215 220

Leu Glu Phe Thr Glu Glu Arg Asp Glu Gly Cys Gly Asp Ala Gly Asp
225 230 235 240

Cys Thr Ser Leu Tyr Ser Pro Gly Ala Glu Asp Ser Asp Ser Leu Ser
245 250 255

Asn Gly Glu Gly Ser Ser Gln Ile Ser Asn Asp Tyr Val Asn Met Thr
260 265 270

Gly Leu Asp Leu Ser Ala Ile Gln Glu Arg Gln Leu Trp Val Ala Phe
275 280 285

Gln Cys Cys Arg Asp Tyr Glu Asn Val Pro Ala Ala Asp Pro Ser Gly
290 295 300

Ser Gln Gln Gln Ala Glu Lys Asp Val Pro Ser Ser Asn Ile Gly His
305 310 315 320

Val Glu Asp Lys Thr Asp Asp Pro Gly Thr His Val Gln Cys Val Lys
325 330 335

Arg Thr Phe Leu Ala Ser Gly Asp Tyr Ala Asp Phe Gln Pro Phe Thr
340 345 350

Gln Ser Glu Asp Ser Gln Met Lys His Arg Glu Glu Met Ser Asn Glu
355 360 365

Asp Ser Ser Asp Tyr Glu Asn Val Leu Thr Ala Lys Leu Gly Gly Arg
370 375 380

Asp Ser Glu Gln Gly Pro Gly Thr Gln Leu Leu Pro Asp Glu
385 390 395

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Ile Leu Trp

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Asp Gln Ile Thr Asn Ile Phe Ser
35 40

<210> 5
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<212> DNA
<213> Artificial sequence

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ccatccctccct ggtcggttgcg gttt 24

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ttccctgtcgca caaggcaaga tgtca 25